

(1) GENERAL INFORMATION:

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(i) APPLICANT: Glimcher, Laurie H.
Hodge, Martin R.

10 (ii) TITLE OF INVENTION: NF-AT-INTERACTING PROTEIN NIP45 AND METHODS
OF USE THEREFOR

(iii) NUMBER OF SEQUENCES: 2

15 (iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: LAHIVE & COCKFIELD
(B) STREET: 60 State Street, suite 510
(C) CITY: Boston
(D) STATE: Massachusetts
(E) COUNTRY: USA

20 (F) ZIP: 02109-1875

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
25 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER:
35 (B) FILING DATE:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Giulio A. DeConti, Jr.
(B) REGISTRATION NUMBER: 31,503
40 (C) REFERENCE/DOCKET NUMBER: HUI-026

(ix) TELECOMMUNICATION INFORMATION:

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(2) INFORMATION FOR SEQ ID NO:1:

50 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1946 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

55 (ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 13..1248

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

5 ACAGTGTGGG AG ATG GCG GAA CCA CTG AGG GGA CGT GGT CCG AGG TCC 48
Met Ala Glu Pro Leu Arg Gly Arg Gly Pro Arg Ser
1 5 10

10 CGC GGT GGC CGA GGC GCT CGG AGA GCC CGA GGC GCC CGT GGC CGG TGT 96
Arg Gly Gly Arg Gly Ala Arg Arg Ala Arg Gly Ala Arg Gly Arg Cys
15 20 25

15 CCT CGC GCC CGG CAG TCT CCG GCT AGG CTC ATT CCA GAC ACC GTG CTT 144
Pro Arg Ala Arg Gln Ser Pro Ala Arg Leu Ile Pro Asp Thr Val Leu
30 35 40

20 GTG GAC TTG GTC AGT GAC AGC GAC GAA GAG GTC TTG GAA GTC GCA GAC 192
Val Asp Leu Val Ser Asp Ser Asp Glu Glu Val Leu Glu Val Ala Asp
45 50 55 60

25 CCA GTA GAG GTG CCG GTC GCC CGC CTC CCC GCG CCG GCT AAA CCT GAG 240
Pro Val Glu Val Pro Val Ala Arg Leu Pro Ala Pro Ala Lys Pro Glu
65 70 75

30 CAG GAC AGC GAC AGT GAC AGT GAA GGG GCG GCC GAG GGG CCT GCG GGA 288
Gln Asp Ser Asp Ser Asp Ser Glu Gly Ala Ala Glu Gly Pro Ala Gly
80 85 90

35 GCC CCG CGT ACA TTG GTG CGA CGG CGG CGG CGG CGG CTG CTG GAT CCC 336
Ala Pro Arg Thr Leu Val Arg Arg Arg Arg Arg Leu Leu Asp Pro
95 100 105

40 GGA GAG GCG CCG GTG GTC CCA GTG TAC TCC GGG AAG GTA CAG AGC AGC 384
Gly Glu Ala Pro Val Val Pro Val Tyr Ser Gly Lys Val Gln Ser Ser
110 115 120

45 CTC AAC CTC ATT CCA GAT AAT TCA TCC CTC TTG AAA CTG TGC CCT TCA 432
Leu Asn Leu Ile Pro Asp Asn Ser Ser Leu Leu Lys Leu Cys Pro Ser
125 130 135 140

50 GAG CCT GAA GAT GAG GCA GAT CTG ACA AAT TCT GGC AGT TCT CCC TCT 480
Glu Pro Glu Asp Glu Ala Asp Leu Thr Asn Ser Gly Ser Ser Pro Ser
145 150 155

55 GAG GAT GAT GCC CTG CCT TCA GGT TCT CCC TGG AGA AAG AAG CTC AGA 528
Glu Asp Asp Ala Leu Pro Ser Gly Ser Pro Trp Arg Lys Lys Leu Arg
160 165 170

60 AAG AAG TGT GAG AAA GAA GAA AAG AAA ATG GAA GAG TTT CCG GAC CAG 576
Lys Lys Cys Glu Lys Glu Lys Lys Met Glu Glu Phe Pro Asp Gln
175 180 185

65 GAC ATC TCT CCT TTG CCC CAA CCT TCG TCA AGG AAC AAA AGC AGA AAG 624
Asp Ile Ser Pro Leu Pro Gln Pro Ser Ser Arg Asn Lys Ser Arg Lys
190 195 200

70 CAT ACG GAG GCG CTC CAG AAG CTA AGG GAA GTG AAC AAG CGT CTC CAA 672
His Thr Glu Ala Leu Gln Lys Leu Arg Glu Val Asn Lys Arg Leu Gln
205 210 215 220

	GAT CTC CGC TCC TGC CTG AGC CCC AAG CAG CAC CAG AGT CCA GCC CTT		720
	Asp Leu Arg Ser Cys Leu Ser Pro Lys Gln His Gln Ser Pro Ala Leu		
	225 230 235		
5	CAG AGC ACA GAT GAT GAG GTG GTC CTA GTG GAA GGG CCT GTC TTG CCA		768
	Gln Ser Thr Asp Asp Glu Val Val Leu Val Glu Gly Pro Val Leu Pro		
	240 245 250		
10	CAG AGC TCT CGA CTC TTT ACA CTC AAG ATC CGG TGC CGG GCT GAC CTA		816
	Gln Ser Ser Arg Leu Phe Thr Leu Lys Ile Arg Cys Arg Ala Asp Leu		
	255 260 265		
15	GTG AGA CTG CCT GTC AGG ATG TCG GAG CCC CTT CAG AAT GTG GTG GAT		864
	Val Arg Leu Pro Val Arg Met Ser Glu Pro Leu Gln Asn Val Val Asp		
	270 275 280		
20	CAC ATG GCC AAT CAT CTT GGG GTG TCT CCA AAC AGG ATT CTT TTG CTT		912
	His Met Ala Asn His Leu Gly Val Ser Pro Asn Arg Ile Leu Leu Leu		
	285 290 295 300		
25	TTT GGA GAG AGT GAA CTG TCT CCT ACT GCC ACC CCT AGT ACC CTA AAG		960
	Phe Gly Glu Ser Glu Leu Ser Pro Thr Ala Thr Pro Ser Thr Leu Lys		
	305 310 315		
30	CTT GGA GTG GCT GAC ATC ATT GAT TGT GTG GTG CTA GCA AGC TCT TCA		1008
	Leu Gly Val Ala Asp Ile Ile Asp Cys Val Val Leu Ser Ser Ser		
	320 325 330		
35	GAG GCC ACA GAG ACA TCC CAG GAG CTC CGG CTC CGG GTG CAG GGG AAG		1056
	Glu Ala Thr Glu Thr Ser Gln Glu Leu Arg Leu Arg Val Gln Gly Lys		
	335 340 345		
40	GAG AAA CAC CAG ATG TTG GAG ATC TCA CTG TCT CCT GAT TCT CCT CTT		1104
	Glu Lys His Gln Met Leu Glu Ile Ser Leu Ser Pro Asp Ser Pro Leu		
	350 355 360		
45	AAG GTT CTC ATG TCA CAC TAT GAG GAA GCC ATG GGA CTC TCT GGA CAC		1152
	Lys Val Leu Met Ser His Tyr Glu Glu Ala Met Gly Leu Ser Gly His		
	365 370 375 380		
50	AAG CTC TCC TTC TTC TTT GAT GGG ACA AAG CTT TCA GGC AAG GAG CTG		1200
	Lys Leu Ser Phe Phe Asp Gly Thr Lys Leu Ser Gly Lys Glu Leu		
	385 390 395		
55	CCA GCT GAT CTG GGC CTG GAA TCC GGA GAT CTC ATC GAA GTC TGG GGC		1248
	Pro Ala Asp Leu Gly Leu Glu Ser Gly Asp Leu Ile Glu Val Trp Gly		
	400 405 410		
60	TGAAGCTCTC ACCCTGTTCG GACGCAAAGC CAAGACATGG AGACAATAGC TCCCAATT		1308
	TTTATTGTGA TTTTCGCC CATAAGGGCT AACAGAAACT GAATTAGAAC TTGTTACT		
	ATTTATTTCT GGTGCTGGGG ATTGAACCCC AGACTATGCA CATGCTAAGG ATGTATGAAG		1428
	TGGAGGCCAA ACCAAGGCAT TACCTTAGC CAGCCTCTAG TAGACTGTAG TGTCAAGCAA		
	GTGGCTACTT GGTAGTTGTG TGGCTCTGTG TATGTTGTG CTGTATTGG CAGCCCCCTGG		1488
	42		1548

GGCACATAGA AGGGACCTTG GCTTCCCTAC CATTTCACGT TCGCTGGTGC CCTTCCCTTC 1608
ATCAGATGAC TTCTGTGAAG CTGCCTATGT TGAGTGTGTT GAACTAAATG AGCTCTGCTT 1668
5 TGGGTGTCCA GGCCTGGGT TTGTGCCGCA GTTGGAGCCA GCAGTGACTT CACTCTGACT 1728
TGGGACTGAG AATGCATTC CTGGTGGAGA CACTCGGGTG CAGAAATATA ACAGAAGGTG 1788
10 ACATACATGC TGAAGCTGAG GACTAGGTG AAAGTTAACG ACGTTGCATT TTCAGCCTTG 1848
GGTATCCTCT CTGCCTGCCA GGACTCTAGC CAGTGTCTGG TACACACTTC TTGGCATGGA 1908
CACCTAGGTC GACGCCGGCG CGATTCCGCC GACTCGAG 1946

15 (2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
20 (A) LENGTH: 412 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Ala Glu Pro Leu Arg Gly Arg Gly Pro Arg Ser Arg Gly Gly Arg
1 5 10 15

30 Gly Ala Arg Arg Ala Arg Gly Ala Arg Gly Arg Cys Pro Arg Ala Arg
20 25 30

Gln Ser Pro Ala Arg Leu Ile Pro Asp Thr Val Leu Val Asp Leu Val
35 40 45

35 Ser Asp Ser Asp Glu Glu Val Leu Glu Val Ala Asp Pro Val Glu Val
50 55 60

40 Pro Val Ala Arg Leu Pro Ala Pro Ala Lys Pro Glu Gln Asp Ser Asp
65 70 75 80

Ser Asp Ser Glu Gly Ala Ala Glu Gly Pro Ala Gly Ala Pro Arg Thr
85 90 95

45 Leu Val Arg Arg Arg Arg Arg Leu Leu Asp Pro Gly Glu Ala Pro
100 105 110

50 Val Val Pro Val Tyr Ser Gly Lys Val Gln Ser Ser Leu Asn Leu Ile
115 120 125

Pro Asp Asn Ser Ser Leu Leu Lys Leu Cys Pro Ser Glu Pro Glu Asp
130 135 140

55 Glu Ala Asp Leu Thr Asn Ser Gly Ser Ser Pro Ser Glu Asp Asp Ala
145 150 155 160

Leu Pro Ser Gly Ser Pro Trp Arg Lys Lys Leu Arg Lys Lys Cys Glu
165 170 175

43

Lys Glu Glu Lys Lys Met Glu Glu Phe Pro Asp Gln Asp Ile Ser Pro
180 185 190

5 Leu Pro Gln Pro Ser Ser Arg Asn Lys Ser Arg Lys His Thr Glu Ala
195 200 205

Leu Gln Lys Leu Arg Glu Val Asn Lys Arg Leu Gln Asp Leu Arg Ser
210 215 220

10 Cys Leu Ser Pro Lys Gln His Gln Ser Pro Ala Leu Gln Ser Thr Asp
225 230 235 240

Asp Glu Val Val Leu Val Glu Gly Pro Val Leu Pro Gln Ser Ser Arg
245 250 255

15 Leu Phe Thr Leu Lys Ile Arg Cys Arg Ala Asp Leu Val Arg Leu Pro
260 265 270

20 Val Arg Met Ser Glu Pro Leu Gln Asn Val Val Asp His Met Ala Asn
275 280 285

His Leu Gly Val Ser Pro Asn Arg Ile Leu Leu Leu Phe Gly Glu Ser
290 295 300

25 Glu Leu Ser Pro Thr Ala Thr Pro Ser Thr Leu Lys Leu Gly Val Ala
305 310 315 320

Asp Ile Ile Asp Cys Val Val Leu Ala Ser Ser Ser Glu Ala Thr Glu
325 330 335

30 Thr Ser Gln Glu Leu Arg Leu Arg Val Gln Gly Lys Glu Lys His Gln
340 345 350

35 Met Leu Glu Ile Ser Leu Ser Pro Asp Ser Pro Leu Lys Val Leu Met
355 360 365

Ser His Tyr Glu Glu Ala Met Gly Leu Ser Gly His Lys Leu Ser Phe
370 375 380

40 Phe Phe Asp Gly Thr Lys Leu Ser Gly Lys Glu Leu Pro Ala Asp Leu
385 390 395 400

Gly Leu Glu Ser Gly Asp Leu Ile Glu Val Trp Gly
405 410